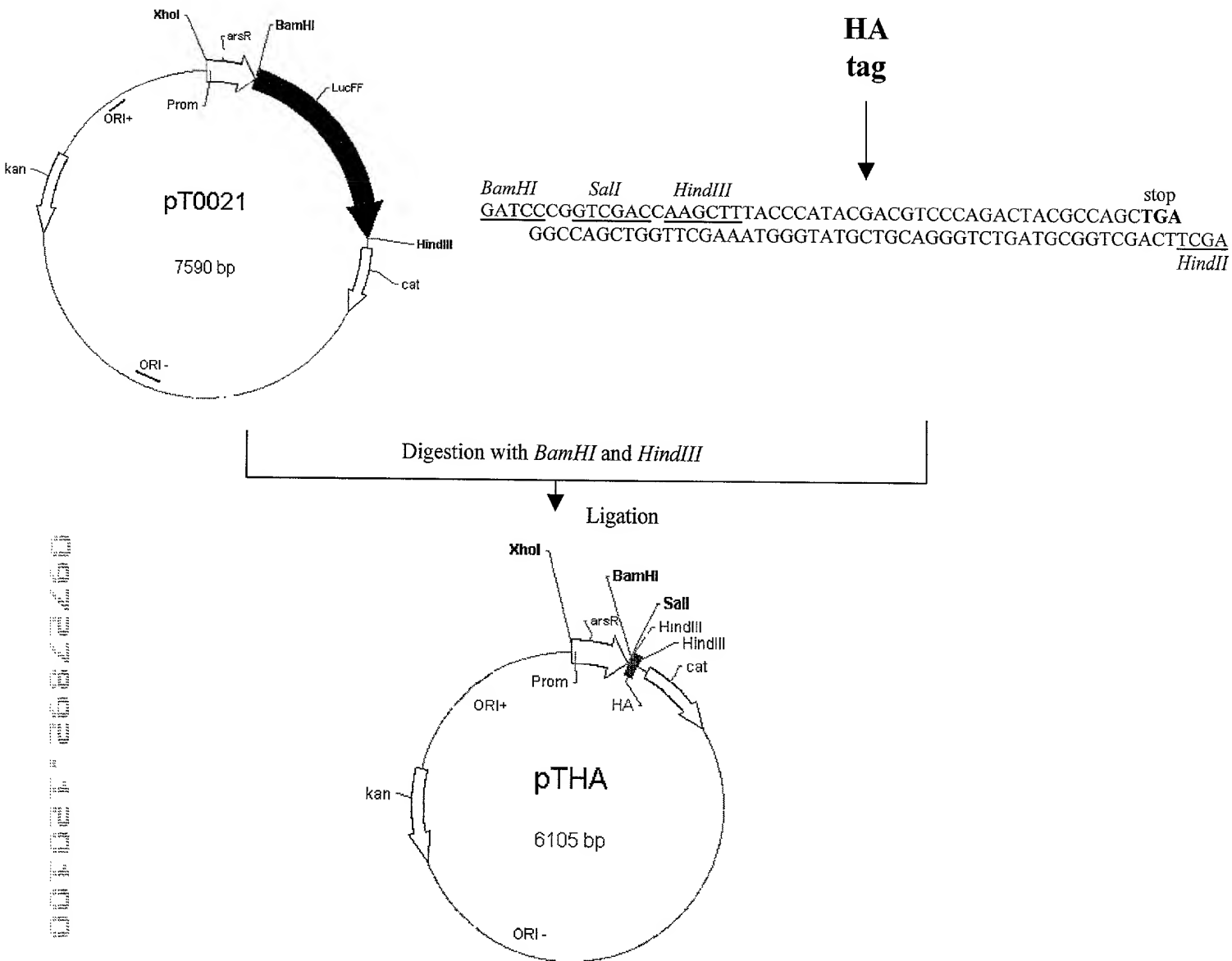


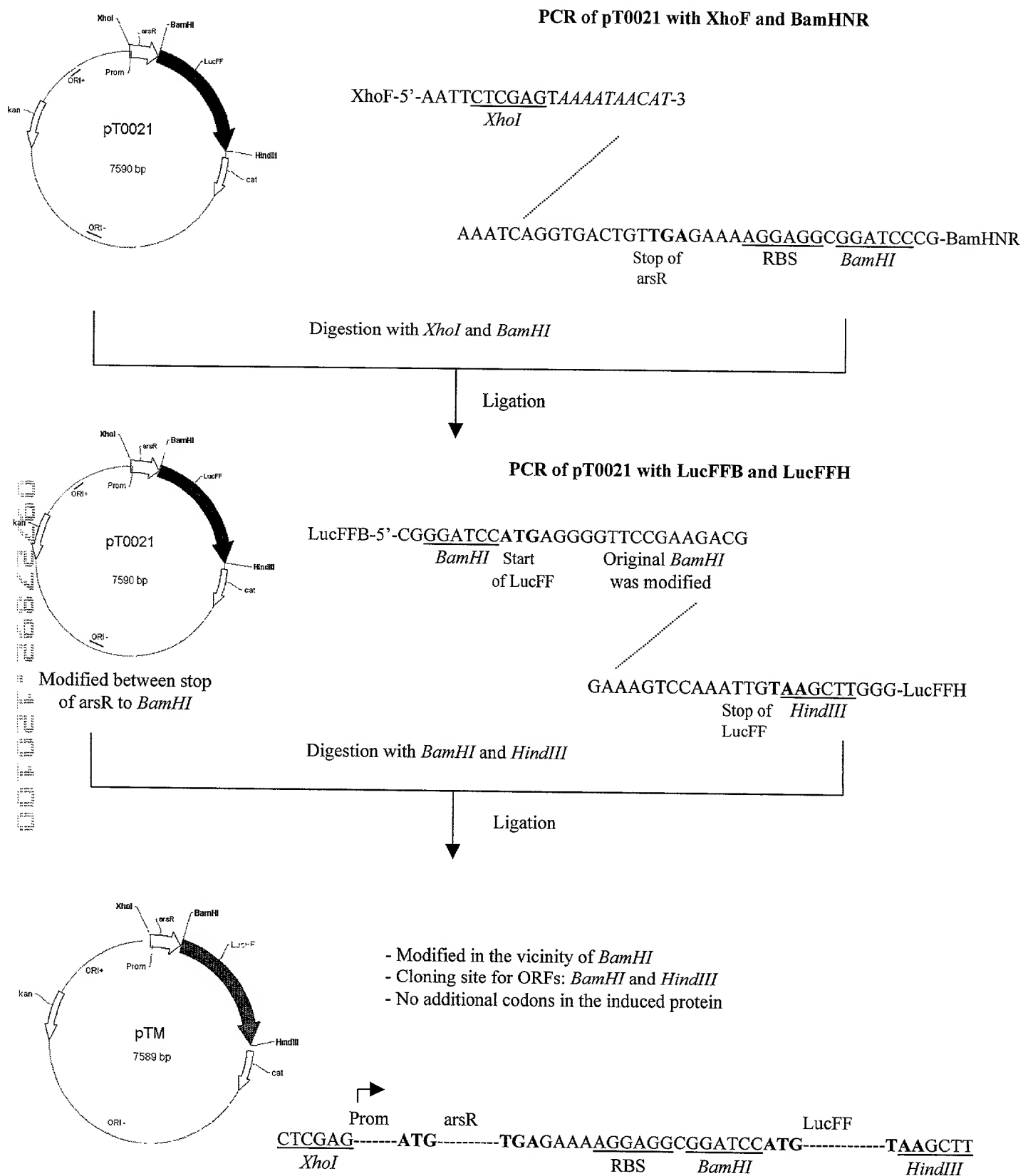
FIGURE 1A

A-



B-

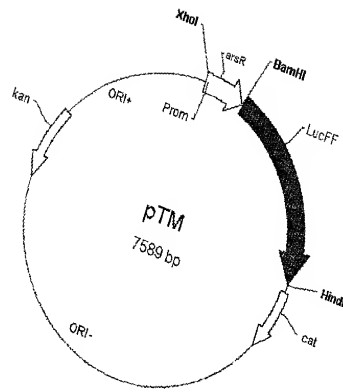
FIGURE 1B



C.

FIGURE 1C

PCR of *Staphylococcus aureus* DNA  
with lacF and LacR

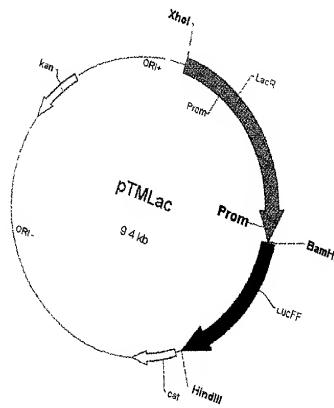


LacF-5'-CCGCTCGAGCTCAAATTCCAAAACAG  
XhoI

GTAAAAAGGAGTCTTATTGGATCCCG-LacR  
BamHI

Digestion with XhoI and BamHI

Ligation



CTCGAG Prom LacR Prom LacA  
XhoI TTG CTA AGGAGTCTTATTGGATCCATG  
BamHI

FIGURE 2A

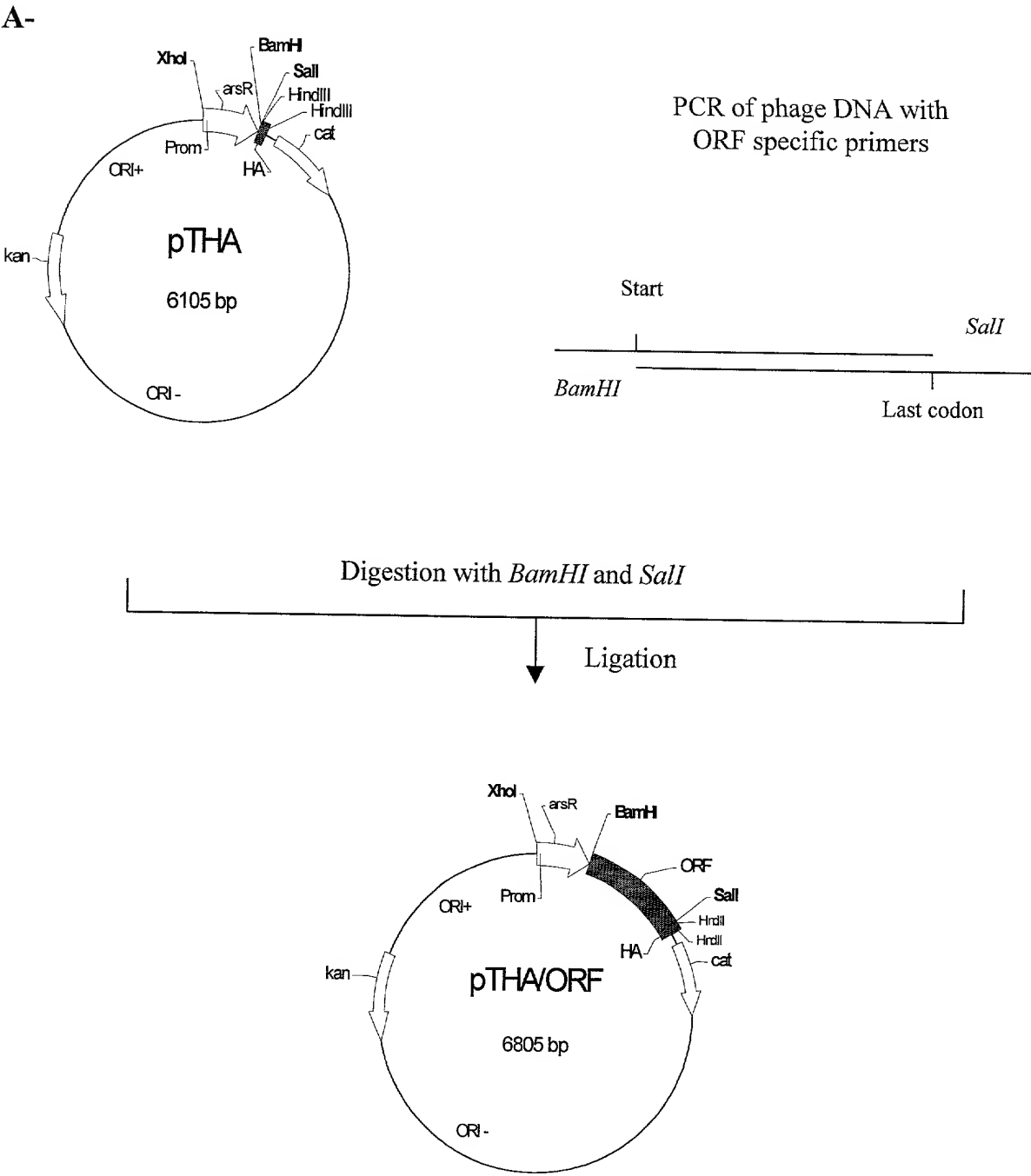
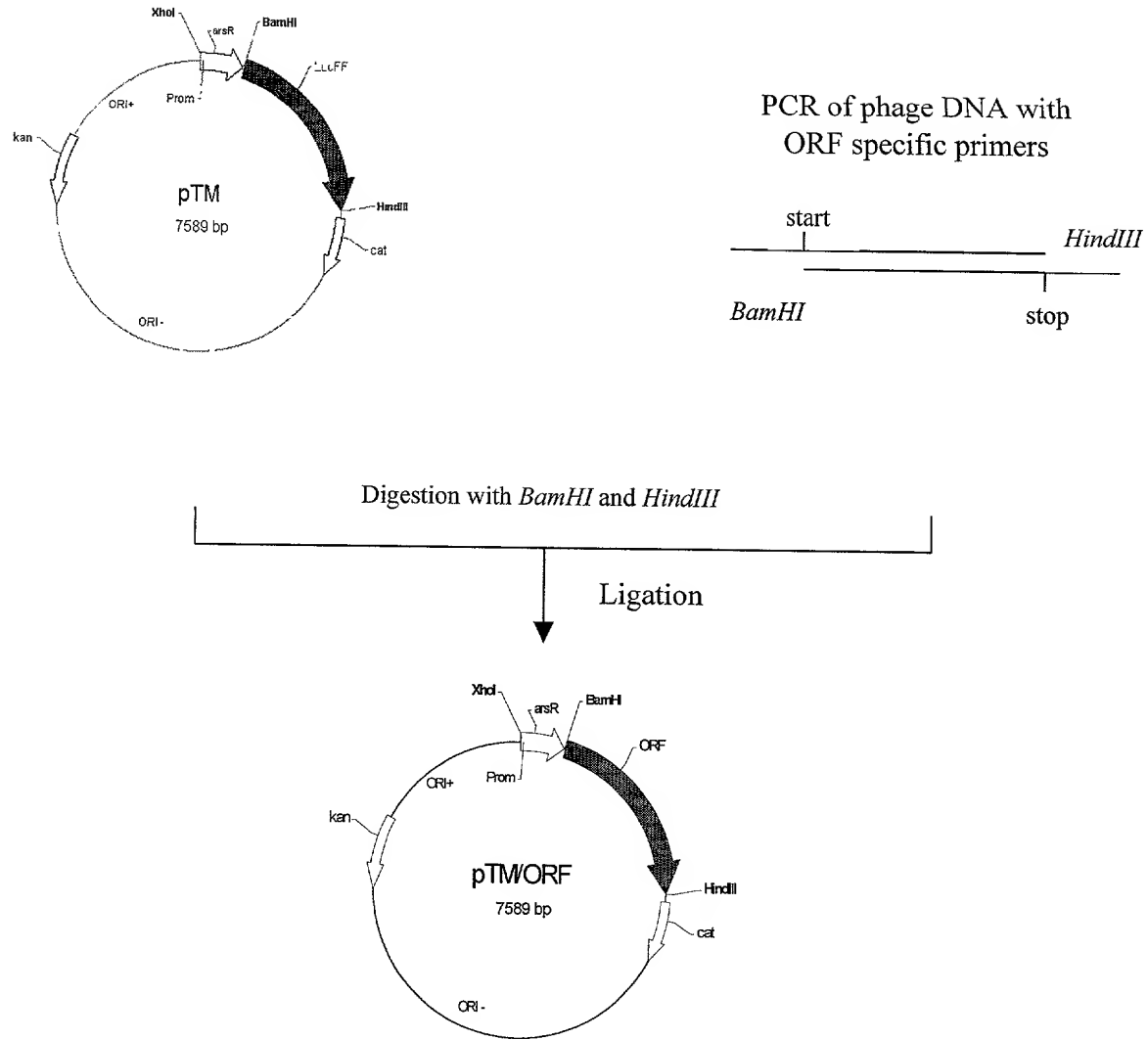


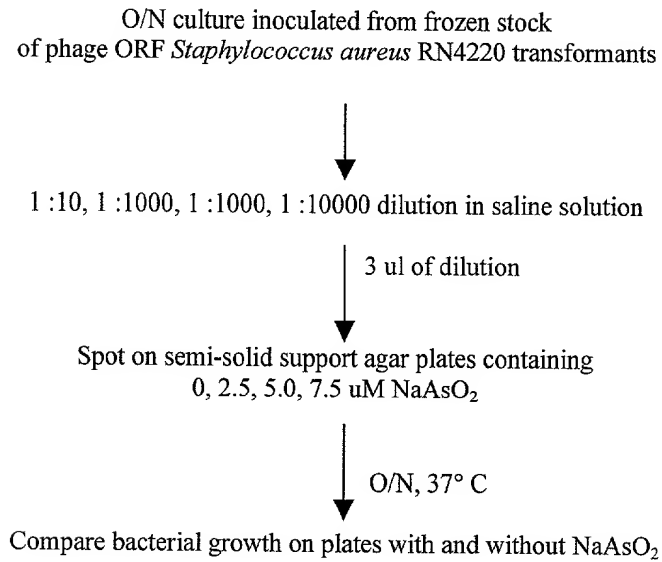
FIGURE 2B

B-



**FIGURE 3**

**A) Functional assay on semi-solid support medium**



**B) Functional assay in liquid medium**

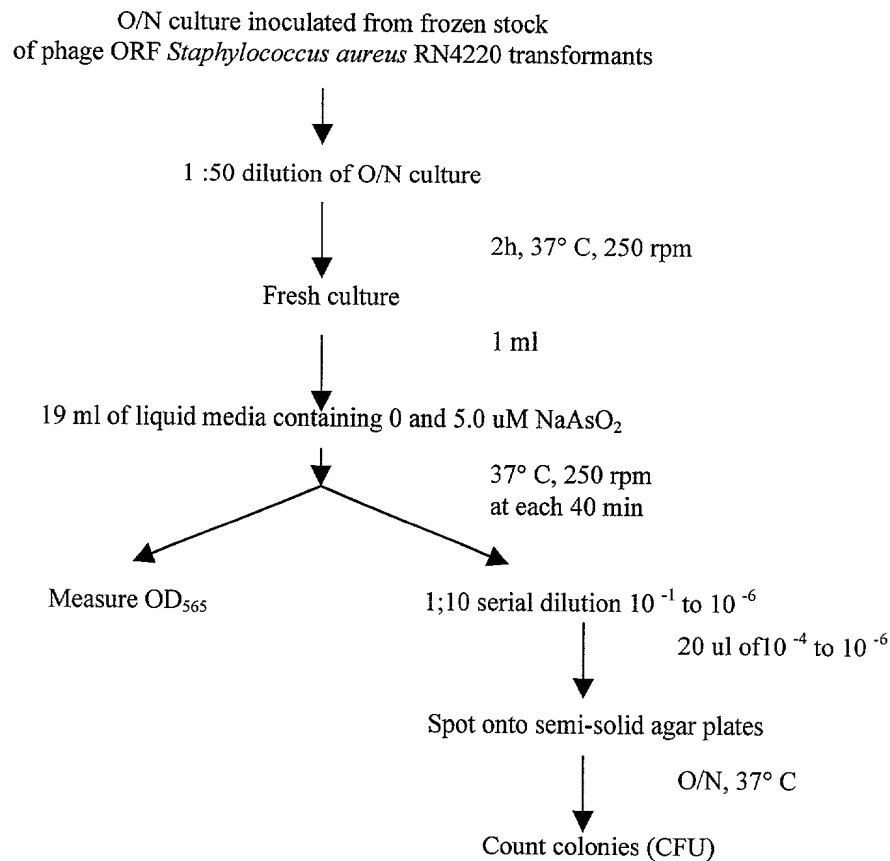


FIGURE 4A

A-

44AHJD ORFs tested for functional analysis

UID	POS
44AHJDORF001	12627..10342
44AHJDORF002	3789..5732
44AHJDORF003	6626..8389
44AHJDORF004	8764..10227
44AHJDORF005	13890..12643
44AHJDORF006	803..2029
44AHJDORF007	2044..3027
44AHJDORF008	3020..3775
44AHJDORF009	5744..6496
44AHJDORF010	14420..13938
44AHJDORF011	15593..15225
44AHJDORF012	8391..8813
44AHJDORF013	14996..14586
44AHJDORF019	9836..9630
44AHJDORF023	6494..6315
44AHJDORF025	15175..14999
44AHJDORF027	12916..13080
44AHJDORF028	9235..9071
44AHJDORF035	13957..13811
44AHJDORF036	10165..10019
44AHJDORF039	1743..1883
44AHJDORF040	9740..9877
44AHJDORF044	12917..12783
44AHJDORF046	4891..5019
44AHJDORF048	15340..15212
44AHJDORF049	5784..5909
44AHJDORF053	3348..3467
44AHJDORF113	199..600
44AHJDORF114	16172..15870
44AHJDORF121	16362..16165
44AHJDORF123	614..796

B-

FIGURE 4B















ORF ID	<i>Staphylococcus aureus</i> transformants	Semi-solid support media		
		Without induction		With induction (5 uM sodium arsenite)
44AHJDORF12	Clone1			
	Clone2			
	Clone3			
44AHJDORF25	Clone1			
	Clone2			
	Clone3			
Control 77ORF30	Clone1			



FIGURE 5A

A-

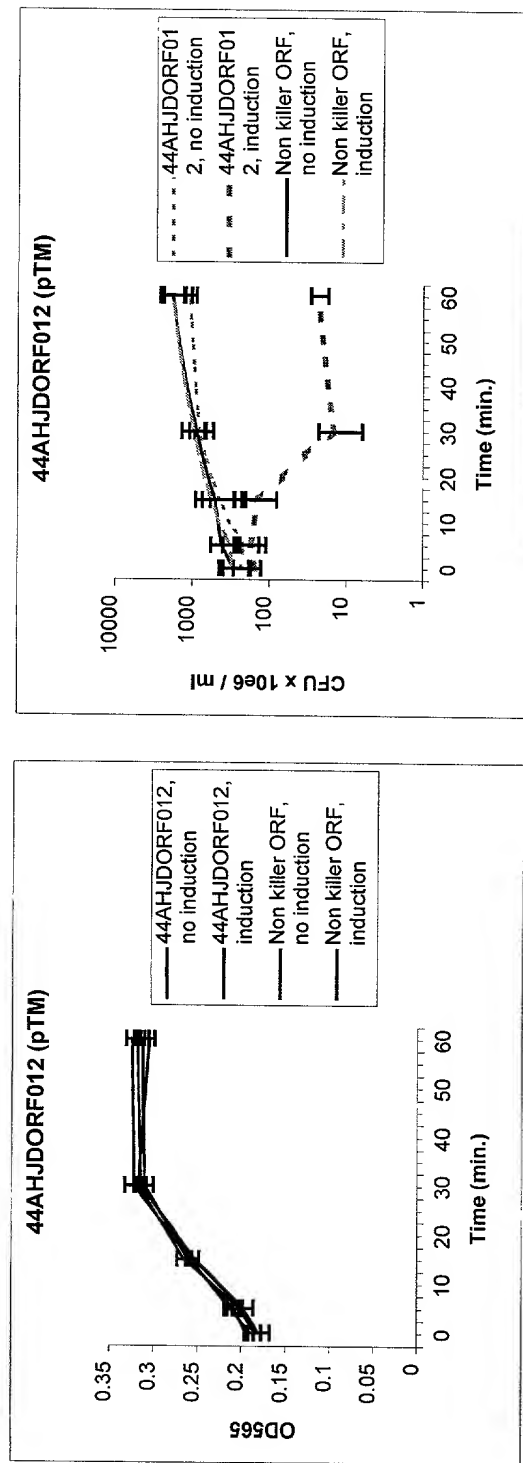
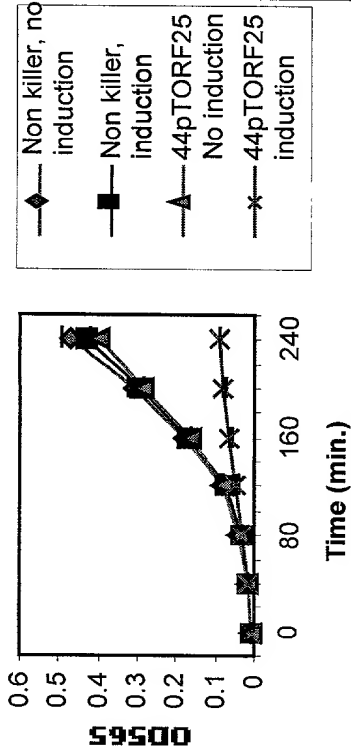
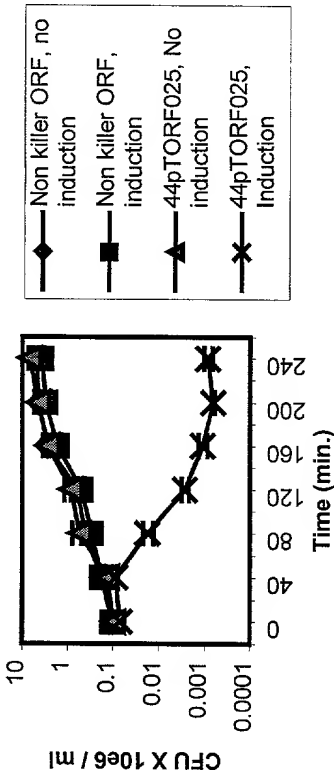


Fig  
.5B

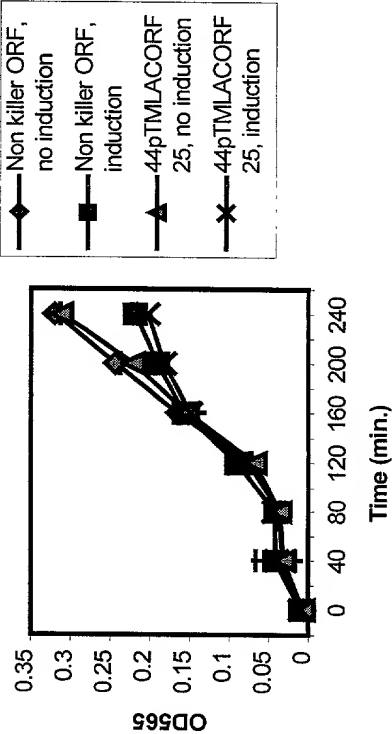
44AHJDORF025 (pT)



44AHJDORF025 (pT)



44AHJD ORF 25 (pTMLac)



44AHJDORF25(pTMLac)

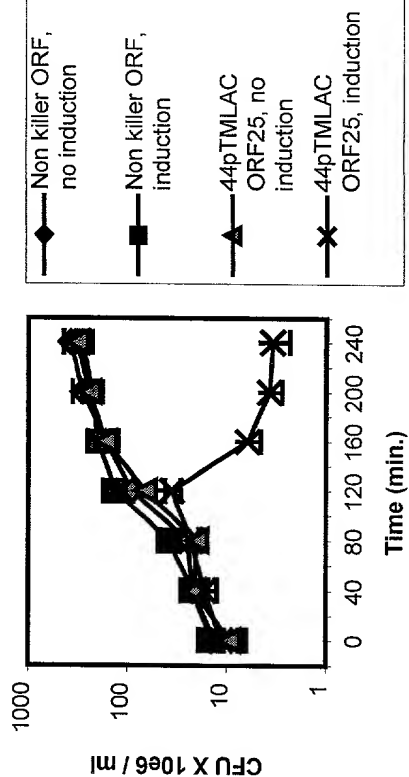


FIGURE 6

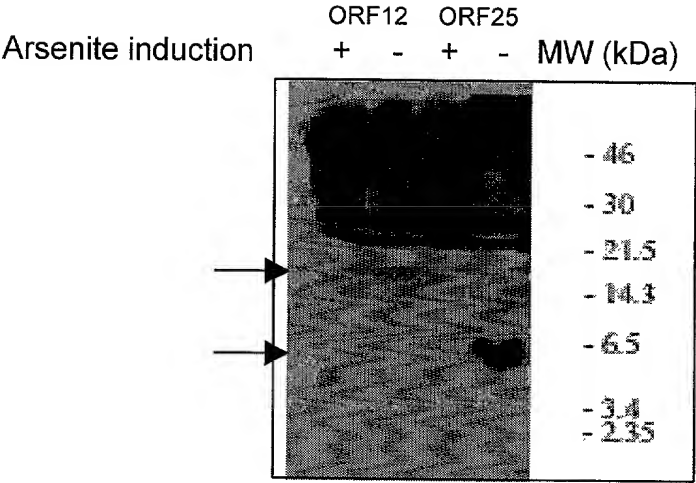


FIGURE 7A

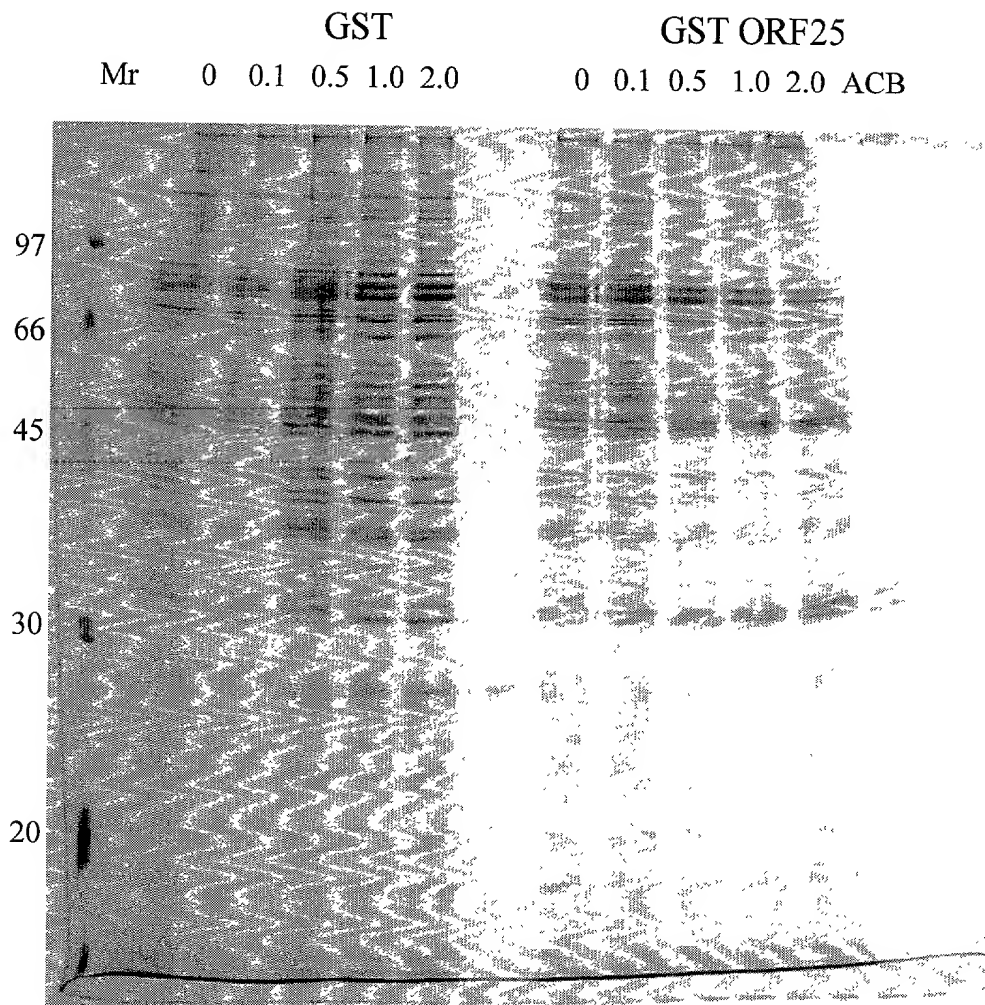
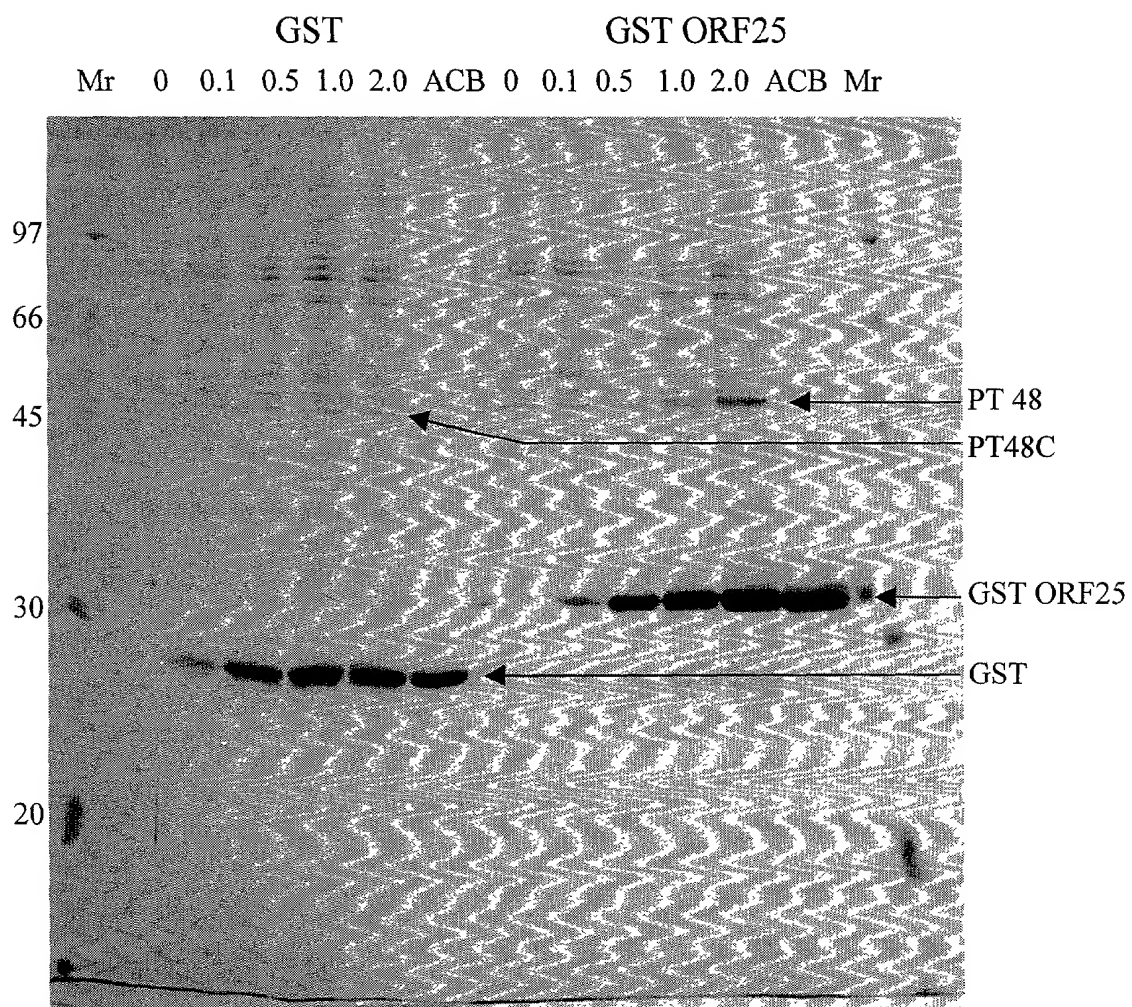


FIGURE 7B

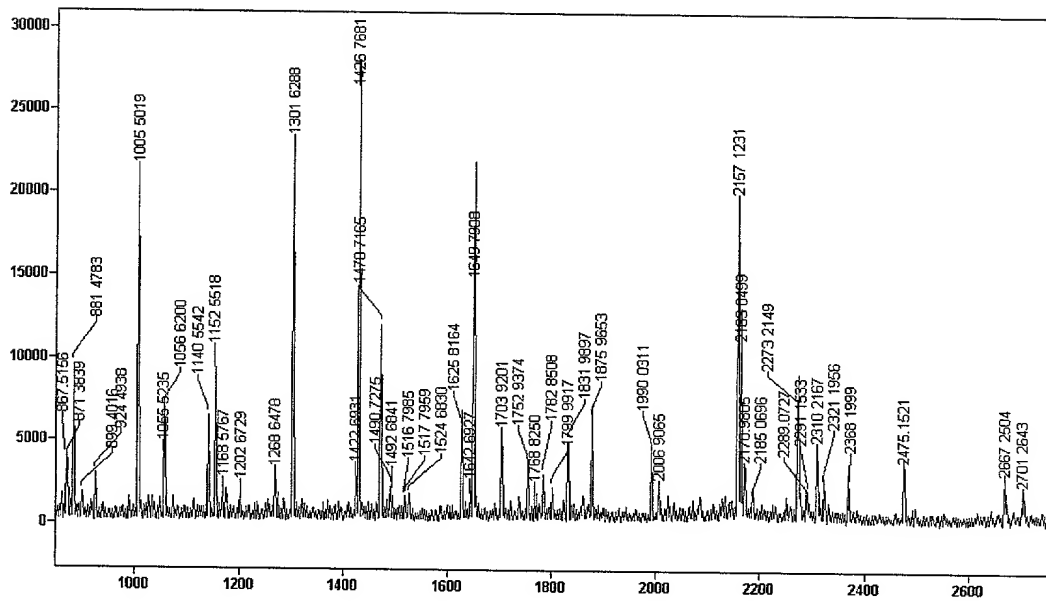


001001-268266

FIGURE 8

Tryptic peptide mass spectrum of 48 kDa interacting protein

(from Figure 1B)



# FIGURE 9

## Identification of PT48 as DNA-directed DNA polymerase III beta.

Details for : PT48

gi|1706496|sp|P50029|DP3B STAAU DNA POLYMERASE III, BETA CHAIN

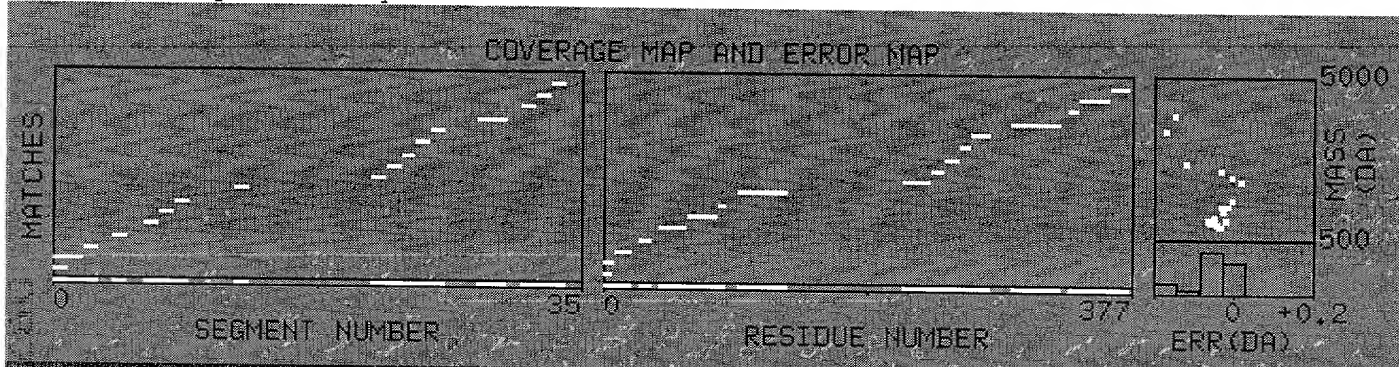
gi|1084187|pir|S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Staphylococcus aureus

Sample ID : PT 48

Number of Measured Peptides : 40

Number of Matched Peptides : 17

Coverage of protein sequence : 68%



Measured Mass(M)	Avg/ Mono	Computed Mass	Error (Da)	Residues Start	To	Missed Cut	Peptide sequence
870.370	M	870.397	-0.027	333	339	0	YMMDALK
880.474	M	880.505	-0.032	82	88	0	FFVDIHK
898.392	M	898.429	-0.037	1	7	0	MMEFTIK
1004.492	M	1004.540	-0.048	235	243	0	VGNVNFISR
1054.514	M	1054.530	-0.016	1	8	1	MMEFTIKR
1055.603	M	1055.658	-0.055	26	35	0	TTLPILTGIK
1151.546	M	1151.586	-0.040	255	263	0	LFPENYEIK
1300.619	M	1300.641	-0.021	244	254	0	LLEGHYPDTR
1425.769	M	1425.782	-0.013	363	375	0	GDDSVTQLIPR
1469.713	M	1469.740	-0.026	9	20	0	DYFITQLNDTIK
1648.781	M	1648.784	-0.003	264	277	0	LSIDNGEYHAIDR
2156.112	M	2156.095	0.017	61	81	0	TVDGEDIVNISETGSVVLPGR
2309.198	M	2309.199	-0.000	40	60	0	EHEVILTGSDSEISIEITIPK
2474.139	M	2474.166	-0.027	214	234	0	IMSDNEEDIDIFFASNQVLEK
2666.266	M	2666.365	-0.099	340	362	0	AIDNDEVEVEFEFGTMKPFILKPK
3577.670	A	3577.809	-0.139	292	326	1	LSTGDDVVELSSTSPEIGTVKEEVDANDVEGCCLK
4033.298	A	4033.421	-0.123	97	132	0	LSTNEQFOTLLTSGHSEFNL SGLDPDQYPLLQVSR

## FIGURE 10

### SEQ ID NO : 1 *Staphylococcus aureus* DnaN nucleotide sequence

ATGATGGAATTCACTATTTAAAAGAGATTATTTTATTACACAATTAAATGACACATTTAAA  
GCTATTTACCAAGAACAACATTACCTATATTAAGTGGTATCAAAATCGATGCGAAAGAA  
CATGAAGTTATATTAAGTGGTTCAGACTCTGAAATTTCAATAGAAATCACTATTCCTAAA  
ACTGTAGATGGCGAAGATATTGTCAATATTTAGAAACAGGCTCAGTAGTACTTCCTGGA  
CGATTCTTTGTTGATATTATAAAAAAATTACCTGGTAAAGATGTTAAATTATCTACAAAT  
GAACAATTCCAGACATTAATTACATCAGGTCATTCTGAATTTAATTTAAGTGGCTTAGAT  
CCAGATCAATATCCTTTATTACCTCAAGTTTCTAGAGATGACGCAATTCAATTGTCGGTA  
AAAGTGCTTAAAAACGTGATTGCACAAACAAATTTTGCAGTGTCCACCTCAGAAACACGC  
CCAGTACTAAGTGGTGTGAAGTGGCTTATACAGAAATGAATTAATATGCACAGCGACT  
GACTCACACCGCTTGGCTGTAAAGAAAGTTCAGTTAGAAGATGTTTCTGAAAAACAAAT  
GTCATCATTCCAGGTAAGGCTTTAGCTGAATTAATAAAATTATGTCTGACAATGAAGAA  
GACATTGATATCTTCTTTGCTTCAACCAAGTTTTATTTAAAGTTGGAAATGTGAACCTT  
ATTTCTCGATTATTAGAAGGACATTATCCTGATACAACACGTTTATTCCCTGAAAACAT  
GAAATTAATAAGTATAGACAATGGGGAGTTTTATCATGCGATTGATCGTGCCTCTTTA  
TTAGCGCGTGAAGGTGGTAATAACGTTATTAATAAGTACAGGTGATGACGTTGTTGAA  
TTGTCTTCTACATCACCAGAAATTGGTACTGTAAAAGAAGAAGTTGATGCAACGATGTT  
GAAGGTGGTAGCCTGAAAATTTCAATCACTCTAAATATATGATGGATGCTTTAAAGCA  
ATCGATAATGATGAGGTTGAAGTTGAATTCCTCGGTACAATGAAACCATTTATTCTAAAA  
CCAAAAGGTGACGACTCGGTAACGCAATTAATTTACCAATCAGAACTTACTAA

### SEQ ID NO : 2 *Staphylococcus aureus* DnaN amino acid sequence

>gi|1084187|pir||S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain -  
*Staphylococcus aureus*

MMEFTIKRDYFITQLNDTLKAISPRITLPILTGIIKIDAKEHEVILTGSDSEISIEITIPKTVDGEDIVNI  
SETGSVVLPGRRFVDIIKKLPKDKVLSTNEQFQTLITSGHSEFNLSGLDPDQYPLLPQVSRDDAIQLSV  
KVLKNVIAQTNFAVSTSETRPVLTGVNWLIIQENELICTATDSHRLAVRKLQLEDVSENKNVLIIPGKALAE  
LNKIMSDNEEDIDIFFASNQVLFKVGNVNFISSLLEGHYPDTTRLFPENYEIKLSIDNGEFYHAIDRASL  
LAREGGNNVIKLSTGDDVVELSSTSPEIGTVKEEVDANDVEGGSLSKISFNKYMDALKKIDNDEVEVEF  
FGTMKPFILKPKGDDSVTQLILPIRTY